

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/058,820A

CRF Edit Date: 4/5/05
Edited by: AE

 Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

✓ Corrected the SEQ ID NO. Sequence numbers edited were:

23,24

 Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

 Deleted: invalid beginning/end-of-file text ; page numbers

 Inserted mandatory headings/numeric identifiers, specifically:

 Moved responses to same line as heading/numeric identifier, specifically:

 Other:



IFW16

RAW SEQUENCE LISTING

DATE: 04/05/2005

PATENT APPLICATION: US/10/058,820A

TIME: 12:49:08

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\04052005\J058820A.raw

4 <110> APPLICANT: Bogan, Jonathan S.
 5 Lodish, Harvey F.
 7 <120> TITLE OF INVENTION: Expression Cloning Method
 10 <130> FILE REFERENCE: 0399.2025-002
 12 <140> CURRENT APPLICATION NUMBER: US 10/058,820A
 13 <141> CURRENT FILING DATE: 2002-01-28
 15 <150> PRIOR APPLICATION NUMBER: US 60/325,651
 16 <151> PRIOR FILING DATE: 2001-09-28
 18 <150> PRIOR APPLICATION NUMBER: US 60/298,963
 19 <151> PRIOR FILING DATE: 2001-06-18
 21 <150> PRIOR APPLICATION NUMBER: US 60/264,816
 22 <151> PRIOR FILING DATE: 2001-01-26
 24 <160> NUMBER OF SEQ ID NOS: 24
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 550
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Mus musculus
 33 <400> SEQUENCE: 1
 34 Met Ala Ala Pro Ala Gly Gly Gly Gly Ser Ala Val Ser Val Leu Ala
 35 1 5 10 15
 36 Pro Asn Gly Arg Arg His Thr Val Lys Val Thr Pro Ser Thr Val Leu
 37 20 25 30
 38 Leu Gln Val Leu Glu Asp Thr Cys Arg Arg Gln Asp Phe Asn Pro Ser
 39 35 40 45
 40 Glu Tyr Asp Leu Lys Phe Gln Arg Thr Val Leu Asp Leu Ser Leu Gln
 41 50 55 60
 42 Trp Arg Phe Ala Asn Leu Pro Asn Asn Ala Lys Leu Glu Met Val Pro
 43 65 70 75 80
 44 Val Ser Arg Ser Arg Glu Gly Pro Glu Asn Ile Val Arg Ile Ala Phe
 45 85 90 95
 46 Gln Leu Asp Asp Gly Ser Arg Leu Gln Asp Ala Phe Cys Ser Arg Gln
 47 100 105 110
 48 Thr Leu Trp Glu Leu Leu Ser His Phe Ala Gln Thr Arg Glu Arg Leu
 49 115 120 125
 50 Gln Gln Leu Gly Glu Lys Thr Pro Val Cys Val Tyr Met Arg Asn Glu
 51 130 135 140
 52 Val Thr Gly Arg Ala Ala Leu Gln Asn Thr Thr Leu Gln Ser Leu Gly
 53 145 150 155 160
 54 Leu Thr Gly Gly Ser Ala Thr Ile Arg Phe Val Ile Lys Gln Cys Asp
 55 165 170 175
 56 Thr Ala Gly Lys Gln Glu Ser Ile Ala Val Arg Ser Lys Ala Pro Gly
 57 180 185 190

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```

58 Ser Pro Val Ser Ser Leu Ser Ala Asp Gln Ala Ser Ser Ser Thr Leu
59      195      200      205
60 Leu Pro Leu Asn Ser Gly Glu Phe Ser Arg Gly Asp Leu Asn His Glu
61      210      215      220
62 Gly Asp Ala Asn Thr Ser Gly Thr Gly Leu Glu Gly Gly Pro Lys Pro
63 225      230      235      240
64 Thr Asp Ala Gln Thr Lys Gln Ser Thr Ser Glu Pro Ala Ser Ala Pro
65      245      250      255
66 Phe Val Pro Phe Ser Gly Gly Gly Gln Arg Leu Gly Gly Pro Ser Ala
67      260      265      270
68 Ser Leu Arg Pro Leu Thr Ser Pro Ser Ala Asn Ser Ser Lys Ser Phe
69      275      280      285
70 Ser Gly Pro Gly Gly Pro Ser Lys Pro Lys Lys Pro Lys Pro Gly Glu
71      290      295      300
72 Glu Pro Gln Gln Glu Pro Glu Pro Pro Val Asp Arg Asp Pro Val Val
73 305      310      315      320
74 Tyr His Pro Asp Leu Glu Asp Leu Leu Gln Pro Trp Pro Ala Glu Val
75      325      330      335
76 Pro Asp Glu Phe Phe Glu Val Thr Val Asp Asp Val Arg Arg Arg Leu
77      340      345      350
78 Ala Gln Leu Lys Ser Glu Arg Lys Arg Leu Glu Glu Ala Pro Leu Val
79      355      360      365
80 Thr Lys Ala Phe Arg Glu Ala Gln Met Lys Glu Lys Leu Glu Arg Tyr
81      370      375      380
82 Pro Lys Val Ala Leu Arg Val Leu Phe Pro Asp Arg Tyr Ile Leu Gln
83 385      390      395      400
84 Gly Phe Phe Arg Pro Ser Glu Thr Val Gly Asp Leu Arg Asp Phe Val
85      405      410      415
86 Arg Ser His Leu Gly Asn Pro Glu Leu Ser Phe Tyr Leu Phe Ile Ala
87      420      425      430
88 Pro Pro Lys Met Val Leu Asp Asp His Thr Leu Thr Leu Phe Gln Ala
89      435      440      445
90 Asn Leu Phe Pro Ala Ala Leu Val His Phe Gly Ala Glu Glu Pro Thr
91      450      455      460
92 Gly Leu Tyr Leu Glu Pro Gly Leu Leu Glu His Thr Val Ser Pro Ser
93 465      470      475      480
94 Thr Ala Asp Val Leu Val Ala Arg Cys Met Ser Arg Ala Ser Gly Ser
95      485      490      495
96 Pro Pro Leu Leu Pro Ala Pro Asp Pro Val Ser Leu Glu Ser Glu Pro
97      500      505      510
98 Ile Ala Glu Asp Gly Ala Leu Gly Pro Pro Glu Pro Ile Gln Gly Thr
99      515      520      525
100 Ala Gln Pro Val Lys Arg Ser Leu Gly Lys Val Pro Lys Trp Leu Lys
101      530      535      540
102 Leu Pro Ala Ser Lys Arg
103 545      550
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 473
108 <212> TYPE: PRT

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RAW SEQUENCE LISTING

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Input Set : A:\PTO.AMC.txt

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```

109 <213> ORGANISM: Mus musculus
111 <400> SEQUENCE: 2
112 Met Val Pro Val Ser Arg Ser Arg Glu Gly Pro Glu Asn Ile Val Arg
113 1 5 10 15
114 Ile Ala Phe Gln Leu Asp Asp Gly Ser Arg Leu Gln Asp Ala Phe Cys
115 20 25 30
116 Ser Arg Gln Thr Leu Trp Glu Leu Leu Ser His Phe Ala Gln Thr Arg
117 35 40 45
118 Glu Arg Leu Gln Gln Leu Gly Glu Lys Thr Pro Val Cys Val Tyr Met
119 50 55 60
120 Arg Asn Glu Val Thr Gly Arg Ala Ala Leu Gln Asn Thr Thr Leu Gln
121 65 70 75 80
122 Ser Leu Gly Leu Thr Gly Gly Ser Ala Thr Ile Arg Phe Val Ile Lys
123 85 90 95
124 Gln Cys Asp Thr Ala Gly Lys Gln Glu Ser Ile Ala Val Arg Ser Lys
125 100 105 110
126 Ala Pro Gly Ser Pro Val Ser Ser Leu Ser Ala Asp Gln Ala Ser Ser
127 115 120 125
128 Ser Thr Leu Leu Pro Leu Asn Ser Gly Glu Phe Ser Arg Gly Asp Leu
129 130 135 140
130 Asn His Glu Gly Asp Ala Asn Thr Ser Gly Thr Gly Leu Glu Gly Gly
131 145 150 155 160
132 Pro Lys Pro Thr Asp Ala Gln Thr Lys Gln Ser Thr Ser Glu Pro Ala
133 165 170 175
134 Ser Ala Pro Phe Val Pro Phe Ser Gly Gly Gly Gln Arg Leu Gly Gly
135 180 185 190
136 Pro Ser Ala Ser Leu Arg Pro Leu Thr Ser Pro Ser Ala Asn Ser Ser
137 195 200 205
138 Lys Ser Phe Ser Gly Pro Gly Gly Pro Ser Lys Pro Lys Lys Pro Lys
139 210 215 220
140 Pro Gly Glu Glu Pro Gln Glu Pro Glu Pro Pro Val Asp Arg Asp
141 225 230 235 240
142 Pro Val Val Tyr His Pro Asp Leu Glu Asp Leu Leu Gln Pro Trp Pro
143 245 250 255
144 Ala Glu Val Pro Asp Glu Phe Phe Glu Val Thr Val Asp Asp Val Arg
145 260 265 270
146 Arg Arg Leu Ala Gln Leu Lys Ser Glu Arg Lys Arg Leu Glu Glu Ala
147 275 280 285
148 Pro Leu Val Thr Lys Ala Phe Arg Glu Ala Gln Met Lys Glu Lys Leu
149 290 295 300
150 Glu Arg Tyr Pro Lys Val Ala Leu Arg Val Leu Phe Pro Asp Arg Tyr
151 305 310 315 320
152 Ile Leu Gln Gly Phe Phe Arg Pro Ser Glu Thr Val Gly Asp Leu Arg
153 325 330 335
154 Asp Phe Val Arg Ser His Leu Gly Asn Pro Glu Leu Ser Phe Tyr Leu
155 340 345 350
156 Phe Ile Ala Pro Pro Lys Met Val Leu Asp Asp His Thr Leu Thr Leu
157 355 360 365
158 Phe Gln Ala Asn Leu Phe Pro Ala Ala Leu Val His Phe Gly Ala Glu

```

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```

159      370      375      380
160 Glu Pro Thr Gly Leu Tyr Leu Glu Pro Gly Leu Leu Glu His Thr Val
161 385      390      395      400
162 Ser Pro Ser Thr Ala Asp Val Leu Val Ala Arg Cys Met Ser Arg Ala
163      405      410      415
164 Ser Gly Ser Pro Pro Leu Leu Pro Ala Pro Asp Pro Val Ser Leu Glu
165      420      425      430
166 Ser Glu Pro Ile Ala Glu Asp Gly Ala Leu Gly Pro Pro Glu Pro Ile
167      435      440      445
168 Gln Gly Thr Ala Gln Pro Val Lys Arg Ser Leu Gly Lys Val Pro Lys
169      450      455      460
170 Trp Leu Lys Leu Pro Ala Ser Lys Arg
171 465      470
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 553
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 3
180 Met Ala Ala Pro Ala Gly Gly Gly Gly Ser Ala Val Ser Val Leu Ala
181 1      5      10      15
182 Pro Asn Gly Arg Arg His Thr Val Lys Val Thr Pro Ser Thr Val Leu
183      20      25      30
184 Leu Gln Val Leu Glu Asp Thr Cys Arg Arg Gln Asp Phe Asn Pro Cys
185      35      40      45
186 Glu Tyr Asp Leu Lys Phe Gln Arg Ser Val Leu Asp Leu Ser Leu Gln
187      50      55      60
188 Trp Arg Phe Ala Asn Leu Pro Asn Asn Ala Lys Leu Glu Met Val Pro
189 65      70      75      80
190 Ala Ser Arg Ser Arg Glu Gly Pro Glu Asn Met Val Arg Ile Ala Leu
191      85      90      95
192 Gln Leu Asp Asp Gly Ser Arg Leu Gln Asp Ser Phe Cys Ser Gly Gln
193      100      105      110
194 Thr Leu Trp Glu Leu Leu Ser His Phe Pro Gln Ile Arg Glu Cys Leu
195      115      120      125
196 Gln His Pro Gly Gly Ala Thr Pro Val Cys Val Tyr Thr Arg Asp Glu
197      130      135      140
198 Val Thr Gly Glu Ala Ala Leu Arg Gly Thr Thr Leu Gln Ser Leu Gly
199 145      150      155      160
200 Leu Thr Gly Gly Ser Ala Thr Ile Arg Phe Val Met Lys Cys Tyr Asp
201      165      170      175
202 Pro Val Gly Lys Thr Pro Gly Ser Leu Gly Ser Ser Ala Ser Ala Gly
203      180      185      190
204 Gln Ala Ala Ala Ser Ala Pro Leu Pro Leu Glu Ser Gly Glu Leu Ser
205      195      200      205
206 Arg Gly Asp Leu Ser Arg Pro Glu Asp Ala Asp Thr Ser Gly Pro Cys
207      210      215      220
208 Cys Glu His Thr Gln Glu Lys Gln Ser Thr Arg Ala Pro Ala Ala Ala
209 225      230      235      240
210 Pro Phe Val Pro Phe Ser Gly Gly Gly Gln Arg Leu Gly Gly Pro Pro

```

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```

211          245          250          255
212 Gly Pro Thr Arg Pro Leu Thr Ser Ser Ser Ala Lys Leu Pro Lys Ser
213          260          265          270
214 Leu Ser Ser Pro Gly Gly Pro Ser Lys Pro Lys Lys Ser Lys Ser Gly
215          275          280          285
216 Gln Asp Pro Gln Gln Glu Gln Glu Gln Glu Arg Glu Arg Asp Pro Gln
217          290          295          300
218 Gln Glu Gln Glu Arg Glu Arg Pro Val Asp Arg Glu Pro Val Asp Arg
219 305          310          315          320
220 Glu Pro Val Val Cys His Pro Asp Leu Glu Glu Arg Leu Gln Ala Trp
221          325          330          335
222 Pro Ala Glu Leu Pro Asp Glu Phe Phe Glu Leu Thr Val Asp Asp Val
223          340          345          350
224 Arg Arg Arg Leu Ala Gln Leu Lys Ser Glu Arg Lys Arg Leu Glu Glu
225          355          360          365
226 Ala Pro Leu Val Thr Lys Ala Phe Arg Glu Ala Gln Ile Lys Glu Lys
227          370          375          380
228 Leu Glu Arg Tyr Pro Lys Val Ala Leu Arg Val Leu Phe Pro Asp Arg
229 385          390          395          400
230 Tyr Val Leu Gln Gly Phe Phe Arg Pro Ser Glu Thr Val Gly Asp Leu
231          405          410          415
232 Arg Asp Phe Val Arg Ser His Leu Gly Asn Pro Glu Leu Ser Phe Tyr
233          420          425          430
234 Leu Phe Ile Thr Pro Pro Lys Thr Val Leu Asp Asp His Thr Gln Thr
235          435          440          445
236 Leu Phe Gln Ala Asn Leu Phe Pro Ala Ala Leu Val His Leu Gly Ala
237          450          455          460
238 Glu Glu Pro Ala Gly Val Tyr Leu Glu Pro Gly Leu Leu Glu His Ala
239 465          470          475          480
240 Ile Ser Pro Ser Ala Ala Asp Val Leu Val Ala Arg Tyr Met Ser Arg
241          485          490          495
242 Ala Ala Gly Ser Pro Ser Pro Leu Pro Ala Pro Asp Pro Ala Pro Lys
243          500          505          510
244 Ser Glu Pro Ala Ala Glu Glu Gly Ala Leu Val Pro Pro Glu Pro Ile
245          515          520          525
246 Pro Gly Thr Ala Gln Pro Val Lys Arg Ser Leu Gly Lys Val Pro Lys
247          530          535          540
248 Trp Leu Lys Leu Pro Ala Ser Lys Arg
249 545          550
252 <210> SEQ ID NO: 4
253 <211> LENGTH: 476
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
257 <400> SEQUENCE: 4
258 Met Val Pro Ala Ser Arg Ser Arg Glu Gly Pro Glu Asn Met Val Arg
259 1          5          10          15
260 Ile Ala Leu Gln Leu Asp Asp Gly Ser Arg Leu Gln Asp Ser Phe Cys
261          20          25          30
262 Ser Gly Gln Thr Leu Trp Glu Leu Leu Ser His Phe Pro Gln Ile Arg

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/058,820A

DATE: 04/05/2005
TIME: 12:49:09

Input Set : A:\PTO.AMC.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 48,57,81,91,96,107,111,122,124,127,130,131,133,134,141
Seq#:10; Xaa Pos. 143,148,152,153,172,174,175,177,178,180,181,182,183,184
Seq#:10; Xaa Pos. 185,186,187,188,190,194,195,198,201,204,205,207,208,212
Seq#:10; Xaa Pos. 216,222,223,224,225,228,231,232,233,234,235,236,239,240
Seq#:10; Xaa Pos. 241,242,243,245,250,251,254,271,272,273,274,280,283,284
Seq#:10; Xaa Pos. 285,288,290,300,302,304,305,306,307,308,309,310,311,312
Seq#:10; Xaa Pos. 313,314,315,316,317,322,324,325,326,327,328,329,330,331
Seq#:10; Xaa Pos. 336,340,346,347,350,355,362,396,417,451,455,462,477,483
Seq#:10; Xaa Pos. 485,495,496,500,508,513,517,518,525,526,527,528,532,535
Seq#:10; Xaa Pos. 539,545

VERIFICATION SUMMARY

DATE: 04/05/2005

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Input Set : A:\PTO.AMC.txt

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L:553 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

L:557 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:561 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:565 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:569 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:573 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:577 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:581 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:585 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:589 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:593 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:597 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:601 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:605 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:609 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:613 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:617 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:621 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:625 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:629 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:633 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:637 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:641 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:645 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:649 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:653 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:657 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:661 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:665 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:669 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:673 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:677 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:681 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:685 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:689 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:693 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:697 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:701 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:705 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:709 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:713 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:717 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:721 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:725 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:729 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:733 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:737 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:741 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

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L:745 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:749 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:753 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10

L:1075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:32

M:341 Repeated in SeqNo=10